



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/798,096

Source: IFNO

Date Processed by STIC: 3/22/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 16798,096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3 ☐ Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4 ☒ Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
  
- 5 ☐ Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7 ☐ Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                            (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                            (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                            This sequence is intentionally skipped  
  
                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence.  
                            <210> sequence id number  
                            <400> sequence id number  
                            000
  
- 9 ☐ Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                            Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                            In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☐ Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ☐ Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
                            Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                            (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☐ PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13 ☐ Misuse of n/Xaa     "**n**" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

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Page 1

## SEQUENCE LISTING

&lt;110&gt; Rea-Min Chu

Ching-Yi Lin

Ya-Wen Hsiao

Kuang-Wen Liao

Submitted file  
could not be processed  
due to numerous errors.

&lt;120&gt; COMPLEX IMMUNO-GENE MEDICAL COMPOSITION FOR INHIBITING TUMOR CELLS

&lt;160&gt;4

&lt;210&gt;1

&lt;211&gt;636

&lt;212&gt; mRNA and PRT

&lt;213&gt; Human

<220> - please insert  
<221> (IL-6) - please insert into section  
<223>

delete, mandatory, <212> has to be either  
DNA, RNA OR PRT, if  
it is both DNA/RNA  
please use type DNA  
and explain in section  
<220>-<223>

&lt;300&gt;

&lt;308&gt; NCBI pubmed Genbank ; Accession No. : NM 000600

<309> ← please insert, mandatory, if <308> is shown  
thank <309> must  
be inserted  
with response.

&lt;400&gt;1

63	78	93	108	
atg aac tcc ttc tcc aca agc gcc ttc ggt cca gtt gcc tcc tcc ctg ggg ctg ctc ctg				
Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu Gly Leu Leu Leu				
1	5	10	15	20
123	138	153	168	120
gtg ttg cct get gcc ttc cct gcc cca gta ccc cca gga gaa gat tcc aaa gat gta gcc				
Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Gly Glu Asp Ser Lys Asp Val Ala Ala				
	25	30	35	40
183	198	213	228	180
gcc cca cac aga cag cca ctc acc tct tca gaa cga att gac aaa cca att cgg tac atc				
Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile				
	45	50	55	60
243	258	273	288	240
ctc gac ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt gaa agc				
Leu Asp Gly Ile tca Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser				
	65	70	75	80
303	318	333	348	300
agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag atg gct gaa aaa gat gga				
Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly				
	85	90	95	100
363	378	393	408	360
tgc ttc caa tct gga ttc aat gag gag act tgc ctg gtg aaa atc atc act ggt ctt ttg				
Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu				
	105	110	115	120
423	438	453	468	

← please  
see item  
# 4  
on error  
summary  
sheet.

gag	ttt	gag	gta	tac	cta	cag	tac	ctc	cag	aac	aga	ttt	gag	agt	agt	gag	gaa	caa	gcc	420
Glu	Phe	Glu	Val	Tyr	Leu	Glu	Tyr	Leu	Gln	Asn	Arg	Phe	Glu	Ser	Ser	Glu	Glu	Gln	Ala	
				125					130					135					140	
<div style="border: 1px solid black; padding: 2px; display: inline-block;">             483                      498                      513                      528           </div>																				
aga	gct	gtg	cag	atg	agt	aca	aaa	gfc	ctg	atc	cag	ttc	ctg	cag	aaa	aag	gca	aag	aat	480
Arg	Ala	Val	Gln	Met	Ser	Thr	Lys	Val	Leu	Ile	Gln	Phe	Leu	Gln	Lys	Lys	Ala	Lys	Asn	
				145					150					155					160	
<div style="border: 1px solid black; padding: 2px; display: inline-block;">             543                      558                      573                      588           </div>																				
cta	gat	gca	ata	acc	acc	cct	gac	cca	acc	aca	aat	gcc	agc	ctg	ctg	acg	aag	ctg	cag	540
Leu	Asp	Ala	Ile	Thr	Thr	Pro	Asp	Pro	Thr	Thr	Asn	Ala	Ser	Leu	Leu	Thr	Lys	Leu	Gln	
				165					170					175					180	
<div style="border: 1px solid black; padding: 2px; display: inline-block;">             603                      618                      633                      648           </div>																				
gca	cag	aac	cag	tgg	ctg	cag	gac	atg	aca	act	cat	ctc	att	ctg	cgc	agc	ttt	aag	gag	600
Ala	Gln	Asn	Gln	Trp	Leu	Gln	Asp	Met	Thr	Thr	His	Leu	Ile	Leu	Arg	Ser	Phe	Lys	Glu	
				185					190					195					200	
<div style="border: 1px solid black; padding: 2px; display: inline-block;">             663                      678                      693           </div>																				
ttc	ctg	cag	tcc	agc	ctg	agg	gct	ctt	cgg	caa	atg									
Phe	Leu	Gln	Ser	Ser	Leu	Arg	Ala	Leu	Arg	Gln	Met			636						
				205					210											

delete, see  
item  
# 4  
on  
error  
summary  
sheet.

<210>2

<211>60

<212>mRNA and PRT

<213>Human

<221>IL-2 Signal Peptide

<300>

<308>NCBI pubmed Genbank : Accession No. : V00564

<309> insert with response

<400>2

atg	tac	agg	atg	caa	ctc	ctg	tct	tgc	att	gca	cta	agt	ctt	gca	ctt	gtc	aca	aac	agt	60
Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	
1				5					10					15					20	

<210>3

<211>342

<212>mRNA and PRT

<213>Human

<221>Partial Sequence Encoding Human IL-15

<300>

delete, same error  
delete  
please insert  
please insert into section <223>  
please move to section <223>

&lt;308&gt;NCBI pubmed Genbank

Accession No. : U14407

same error

&lt;309&gt; ← pls insert

&lt;400&gt;3

aac	tgg	gtg	aat	gta	ata	agt	gat	ttg	aaa	aaa	att	gaa	gat	ctt	att	caa	tct	atg	cat	60
Asn	Trp	Val	Asn	Val	Ile	Ser	Asp	Leu	Lys	Lys	Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	
1				5					10					15					20	
att	gat	gct	act	tta	tat	acg	gaa	agt	gat	gtt	cac	ccc	agt	tgc	aaa	gta	aca	gca	atg	120
Ile	Asp	Ala	Thr	Leu	Tyr	Thr	Glu	Ser	Asp	Val	His	Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	
				25					30					35					40	
aag	tgc	ttt	ctc	ttg	gag	tta	caa	gtt	att	tca	ctt	gag	tcc	gga	gat	gca	agt	att	cat	180
Lys	Cys	Phe	Leu	Leu	Glu	Leu	Gln	Val	Ile	Ser	Leu	Glu	Ser	Gly	Asp	Ala	Ser	Ile	His	
				45					50					55					60	
gat	aca	gta	gaa	aat	ctg	atc	atc	cta	gca	aac	aac	agt	ttg	tct	tct	aat	ggg	aat	gta	240
Asp	Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala	Asn	Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	
				65					70					75					80	
aca	gaa	tct	gga	tgc	aaa	gaa	tgt	gag	gaa	ctg	gag	gaa	aaa	aat	att	aaa	gaa	ttt	ttg	300
Thr	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	
				85					90					95					100	
cag	agt	ttt	gta	cat	att	gtc	caa	atg	ttc	atc	aac	act	tct							342
Gln	Ser	Phe	Val	His	Ile	Val	Gln	Met	Phe	Ile	Asn	Thr	Ser							
				105					110											

&lt;210&gt;4

&lt;211&gt;402

&lt;212&gt;mRNA and

PRT

&lt;213&gt; Artificial Chimeric Sequence

&lt;220&gt;

&lt;221&gt; IL-2SP/IL-15MP

&lt;223&gt; Artificial Chimeric Sequence Encoding IL-2SP/IL-15MP

&lt;300&gt;

&lt;308&gt;NCBI pubmed Genbank

IL-2 Accession No. : V00564

IL-15 Accession No. : U14407

please insert  
dates for each  
accession No.

&lt;309&gt; ← insert

&lt;400&gt;4

atg	tac	agg	atg	caa	ctc	ctg	tct	tgc	att	gca	cta	agt	ctt	gca	ctt	gtc	aca	aac	agt	60
Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	
1				5					10					15					20	
Sequence encoding IL-2signal peptide																				
aac	tgg	gtg	aat	gta	ata	agt	gat	ttg	aaa	aaa	att	gaa	gat	ctt	att	caa	tct	atg	cat	120
Asn	Trp	Val	Asn	Val	Ile	Ser	Asp	Leu	Lys	Lys	Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	
				25					30					35						

delete

